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35. The method of Claim 1 wherein said genetic locus has at least four alleles.
- 49  
36. The method of Claim 1 wherein said genetic locus has at least eight alleles.
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38. The method of Claim 37 wherein said non-coding region sequence is not more than about one kilobase in length.

REMARKS

Reconsideration of the application in light of the amendments above and the following remarks is respectfully requested. Claims 1-16, 21-27, 37, and 39-43 were pending in the application. Claims 28-34 have been withdrawn pursuant to a restriction requirement. Claims 1, 7, 21, 26, and 37 have been amended. Claims 17-20, 35, 36, and 38 were added. Claims 1-27 and 35-43 are now pending.

Support for the amendments is as follows. The Specification was amended to update the status of related applications, as requested by the Examiner.

Support for the amendments to Claims 1, 7, and 26 is found in the preamble of the claims. Claim 21 was amended as suggested by the Examiner by reciting that the primer sites (defined as the area of target DNA to which a primer hybridizes at page 11, lines 17-18), rather than the primers, are located in the specified regions. Support for the amendment to Claim 37 is present in the original wording of the claim.

Newly added Claims 17-20, 35, 36, and 38 were canceled without prejudice to place the application in condition for allowance in response to the Office Action mailed December 13, 1993, indicating that Claims 1-16, 21-27, 37, and 39-43 were allowed. Since the Office Action mailed January 13, 1994, removed the indication that the claims were allowed, those claims have been added. Those claims were present in the application as filed.

No new matter is added by any of the amendments.

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Rejection of Previously Allowed Claims

The Office Action mailed December 13, 1993, indicated that Claims 1-16, 21-27, 37, and 39-43 were allowed. In response to that Office Action, Applicant canceled each of the pending claims which were not allowed, thus placing the case in condition for allowance. MPEP 706.04 states:

A claim noted as allowable shall thereafter be rejected only after the proposed rejection has been submitted to the primary examiner for consideration of all the facts and approval of the proposed action.

PREVIOUS ACTION BY DIFFERENT EXAMINER

Full faith and credit should be given to the search and action of a previous examiner unless there is a clear error in the previous action or knowledge of other prior art. In general, an examiner should not take an entirely new approach or attempt to reorient the point of view of a previous examiner, or make a new search in the mere hope of finding something.

Because it is unusual to reject a previously allowed claim, the examiner should point out in his or her letter that the claim now being rejected was previously allowed by using Form Paragraph 7.50.

In the Office Action mailed January 13, 1994, the Amendment filed December 22, 1993, was entered and all of the pending claims (all of which were previously indicated as allowable) were rejected. No statement that the claims now being rejected were previously allowed, nor any explanation of the basis for rejecting the allowed claims was present in the Office Action. In addition, the Supervisory Patent Examiner did not sign the Office Action. Furthermore, the Examiner apparently performed a new search since an additional reference which did not result in any art-based rejections was cited. The Office Action also included numerous grounds for rejection which either had never been raised or had been raised and overcome in this or the parent application. None of the new rejections were based on prior art, and many were technical rejections. The Office Action thus did not give full faith and credit to the search and action of previous examiners of the application. Those previous examiners included Examiner Moscovitz who was present at a personal interview and allowed

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the claims in the parent application which issued as U.S. Patent No. 5,192,659. The present Office Action thus included objections to the specification and rejections based on new matter, indefiniteness, and lack of enablement for failure to teach how to practice the invention which were not present in the case following Examiner Moscovitz's review of the application. In addition, Examiner Tran removed the 35 U.S.C. §112, first paragraph, enablement rejection for lack of a sufficient demonstration of operability of the method in light of the Declarations of Drs. Gresshoff and Hood.

Applicant's Attorney respectfully requests that the Examiner extend full faith and credit to the Office Action dated December 13, 1993. Alternatively, Applicant's Attorney respectfully requests that the Examiner extend full faith and credit at least to the determination of Examiners Moscovitz and Yuan at the close of prosecution of the parent application. In particular, Applicant's Attorney requests that Examiner Sisson withdraws all of the rejections for the claims pending at the close of prosecution with the exception of the enablement rejection based on insufficient evidence of operability and that Examiner Sisson considers the evidence of record in this application which demonstrates that the method is operable for the breadth of the pending claims and allows the pending claims.

#### Objections

The objection to the Specification is overcome in part and in part traversed. The Specification was objected to on three bases. First, the Specification, particularly pages 3-7 and 24, was objected to for failure to point out the pertinent passages of references which were incorporated by reference. It is believed that the pertinent pages of the application are 5-7 and 24, rather than 3-7 and 24, since there are no citations to references on pages 3 and 4.

With the exception of the articles related to the cystic fibrosis gene, each of the cited references describes various procedures which can be used in the method of this invention. For example, U.S. Patent No. 4,683,195 (page 5, lines 5-14) describes the polymerase chain reaction sequence amplification method which can be used in the method of the claimed invention. The references are generally pertinent in describing such techniques and do not contain passages of particular relevance. The articles related to the cystic fibrosis gene are also generally relevant as the methods of the invention can be used to determine alleles of the gene. Therefore, since the articles do not contain particularly pertinent passages, but rather are generally relevant, withdrawal of the rejection is respectfully requested.

Second, the objection to the Specification for failure to update the status of related applications is moot in light of the amendments to the application.

Third, the Specification was objected to for including legal phraseology in the Abstract. In particular, use of the term "comprises" was found objectionable. The term "comprises" is a common English word which means "to include or contain" and therefore is believed to be appropriately used in the Abstract. However, the term has been replaced by the term "includes" as requested by the Examiner.

Therefore, withdrawal of all of the objections is respectfully requested.

Rejection under 35 U.S.C. §112, first paragraph (new matter)

The objection to the Specification and rejection of Claims 1-16 under 35 U.S.C. §112, first paragraph, is respectfully traversed. The Examiner stated that Claims 1-16 are not supported by the original disclosure "for 'non-coding regions'".

The Examiner argued that despite the clear definition of how the term "intron" was being used throughout the application, the term "non-coding" is new matter. In particular, the Examiner stated:

In reviewing said page 10, lines 29-33, is (*sic*, it) is clearly evident that the use of the term "non-coding" was being made in reference to an intron. The phrase does not provide support for "non-coding" regions in general. . . . In reviewing the specification, support for the use of "intron" has been located and it (*sic*, it is) readily apparent that the non-coding region contemplated is that associated with introns, not that associated with generic (*sic*, genetic) material in a general sense. (page 3)

First, it is well established that a patentee can be his own lexicographer. The clear definition in the specification which states the meaning for the term intron as used throughout the application provides clear support for the term. Second, that the Examiner can point out examples that use intervening sequences does not mean that other non-coding regions are not contemplated. An Applicant is not required to provide any working examples. Therefore, examples using non-coding region sequences other than introns are not required to support the term "non-coding."

Furthermore, in addition to the clear definition of the term "intron," the specification clearly contains evidence that non-coding regions other than introns are contemplated. In fact there are numerous references throughout the application to non-coding regions other than introns. For example, page 16, lines 27-31 refers to "highly conserved intron sequences (e.g., promoters, enhancers, or other regulatory regions). Clearly, such regulatory regions are generally found in the 5' flanking region of a gene rather than in intervening sequences. At page 17, lines 20-25, the specification refers to introns "located in the downstream or upstream gene flanking regions or even in an intervening sequence in another genetic locus," further supporting the breadth of the definition of the term "intron."

Finally, Claims 1-16 were pending at the close of prosecution of the parent application and were not rejected as including new matter. Examiner Moscovitz and Examiner Yuan permitted entry of the claims and, further, allowed the parent application (now U.S. Patent No. 5,192,659) using the term "non-coding" in the issued claims. Deference to the determinations of the prior examiners should be accorded. The Examiner's raising of the issue of new matter at this point in prosecution not only raises issues that should have been raised in an earlier Office Action, but calls the appropriateness of the determinations by Examiners Moscovitz and Yuan in the parent application into question. This action is clearly inappropriate and withdrawal of the rejection is respectfully requested.

In summary, in light of the clear support for the term "non-coding", withdrawal of the rejection of Claims 1-16 for new matter is respectfully requested.

Rejection under 35 U.S.C. §112, first paragraph (enablement)

The objection to the specification and rejection of Claims 1-13, 15, 16, 37, and 39-41 under 35 U.S.C. §112, first paragraph, for lack of enablement is respectfully traversed. The Examiner states several grounds as the basis for the rejection, as follows:

The specification does not provide sufficient enablement such that one of skill in the art would be able to detect at least one coding region allele of a multi-allelic genetic locus where the genomic DNA can be derived from any source. In particular, the specification has not provided guidance as to how one is to predetermine what types of primers (sequence length and composition) are to be used given the generic applicability of the claimed method to a variety of loci. This aspect is further complicated when one considers that a given locus may well be comprised of a cluster of alleles (*exempli gratia*, the HLA Class II locus DQA1 is comprised of 8 alleles and the DPB locus is comprised of 24 alleles).

The specification is not enabling for the generation and use of primers that would be of sufficient length such that they permit the spanning of virtually any intronic sequence. (page 4)

First, the application provides pages of guidance as to the selection of primers of appropriate length and composition. In particular, page 13, line 15 through page 24, line 36, describes the selection of primers, including sections describing the length of the resultant amplified sequence, the location of the amplified sequence, and the required length and sequence homology of primers. In general, a non-coding region of DNA containing a unique sequence which is present in only one allele of a genetic locus can be amplified and analyzed to determine the presence of the region in the sample. For example, the sequence can be analyzed to determine a change in the length of the sequence, gain or loss of a restriction site, or substitution of a nucleotide (see page 19, lines 30-35). The amplified sequence can be selected based on a difference between alleles of a locus determined by comparing non-coding region sequences of alleles of the locus, or suitable differences can be empirically determined without determining the non-coding region sequences of alleles of the locus. See Example 3 which displays both length differences which distinguish some groups of haplotypes and use of digestion products of amplified sequences of about 700-800 bp which distinguish haplotypes of the DQA locus. Such patterns can be produced and analyzed without knowing the complete sequence of the non-coding region being amplified.

Second, methods of selecting primers to amplify a selected region of DNA are well known and within the level of skill in the art and were within the level of skill in the art at the time the application was filed. It is clear from the numerous publications analyzing various genetic loci of various species that one of ordinary skill can determine the required length and sequence homology of primers to amplify a selected region of genomic DNA. Furthermore, the patents and articles related to selection of primers for amplification of DNA which were incorporated by reference indicate the level of skill in

amplifying DNA. Therefore, it is clear that one of ordinary skill could select primers to amplify regions of non-coding sequences that distinguish alleles in light of the teachings of the application and the level of skill in the art.

The Examiner's reference to the number of alleles of the HLA loci is not understood since Applicant exemplified the method using the HLA loci and has an issued patent (the parent application) related to analysis of HLA loci. The only issue in this application at the close of prosecution of the parent application was whether the method was operable for loci generally since the exemplification was for HLA loci. There was no issue of whether one of skill could practice the method by selecting appropriate primers at the close of prosecution.

The Examiner's statement that one cannot generate and use primers that would be of sufficient length such that they permit the spanning of virtually any intronic sequence appears to be based on the use of the term "intron spanning." At page 11, lines 31-33, the term "intron spanning primers" is defined as "a primer pair that amplifies at least a portion of one intron." Therefore, since the primers amplify a portion of an intron, it is irrelevant whether the intron is 200 nucleotides or 10 kilobasepairs in length since the method only need amplify a portion of the intron.

Finally, according to MPEP 707.07(g), piecemeal examination should be avoided as much as possible, and the Examiner ordinarily should reject each claim on all valid grounds available, avoiding, however, undue multiplication of references. Furthermore, major technical rejections should be applied where appropriate even though there may be seemingly sufficient rejection on the basis of prior art. Therefore, the Patent Office requires an examiner to give a complete first Office Action which includes raising all grounds for rejection in that action.

Although the present examiner has not examined the application prior to the present Office Action, there were two previous actions in the present application. Furthermore, at the close of prosecution of the parent application which resulted in issuance of U.S. Patent No. 5,192,659, the only remaining issue with regard to the claims rejected for enablement in the present Office Action was lack of enablement based on an insufficient demonstration of operability of the method outside the HLA genes. Examiners Moscovitz and Yuan agreed that one of ordinary skill could perform the method on any genetic locus. However, they believed that the record did not demonstrate that the method would work outside the HLA loci. At the close of prosecution of the parent application, the Examiners agreed that Applicant should submit evidence that the method was applicable to genetic loci, generally, to obtain allowance of the rejected claims. The careful review of the application by Examiners Moscovitz and Yuan, following a personal interview, should be given due deference by the present Examiner.

In particular, at the close of prosecution of the parent application, Applicant proposed submitting additional data regarding a conserved locus. However, the Examiners in the parent application were uncertain whether such additional data by itself would convince the Examiners that the method was generally applicable. Therefore, the Examiners indicated that additional data together with the declaration of an expert who carefully explained why the additional data demonstrated the general applicability of the method should be submitted. After analyzing the reasoning by the expert, the Examiners would decide if the declaration was sufficient to overcome the rejection.

If the present rejection is based on lack of demonstrated applicability to loci generally, Applicant has submitted Declarations by experts attesting to the general applicability

of the method. More specifically, the Declaration of Dr. Peter Gresshoff was submitted together with a Preliminary Amendment. In his Declaration, Dr. Gresshoff described data that convinced Dr. Gresshoff that the present method was generally applicable to eukaryotic loci. The data related to an intergenic region near the soybean supernodulation (NTS) locus, a conserved locus in a plant. Dr. Gresshoff presented reasons explaining why the soybean data together with the HLA data presented by Dr. Simons was convincing. Dr. Gresshoff was working in that intergenic region of the soybean genome and found sequence polymorphisms in a region not greater than one kilobase that contained informative polymorphisms which were indicative of the soybean co-cultivar. Since Dr. Gresshoff had no reason to believe the region was anything other than typical of intergenic regions of the soybean genome or of the genomes of other plants, he believes that "there is no reason to expect that other regions of the soybean genome or any other plant genome would be different."

In addition, Dr. Gresshoff stated that although the NTS gene is a conserved gene, "the same correlation of non-coding region polymorphisms with coding region polymorphisms which is present in the HLA genes is also present in the soybean NTS gene." Dr. Gresshoff stated that when he only was aware of the HLA data, he was concerned that the phenomenon could be related to members of the immunoglobulin super-gene family or to gene families with high coding region variability. Any such concerns were clearly eliminated by observing the same phenomenon in a conserved gene.

Dr. Gresshoff also stated that in addition to demonstrations of this non-coding region micro-heterogeneity in both highly polymorphic and conserved genes, the data were obtained in humans and in soybeans. "Clearly, this indicates that the phenomenon is not limited to humans or even animals." Dr. Gresshoff believes that the presence of non-coding region

polymorphisms that are indicative of coding region polymorphisms (alleles) in such phylogenetically distant species indicates that the phenomenon is present in eukaryotic genomes generally. In addition, the sequence variations found by Dr. Gresshoff were in an intergenic region, rather than in an intervening sequence. The useful non-coding region sequences thus are not limited to those associated with a genetic locus, such as the introns or flanking regions of the gene.

The Declaration of Dr. Leroy E. Hood was submitted on September 24, 1993. Dr. Hood is a well known expert in the field of genetics. In his Declaration, Dr. Hood described that he sequenced a 100 kilobase region of the Alpha Delta T-cell receptor gene in both mouse and man. Ninety-five percent of the sequenced region was non-coding. Dr. Hood found the homology between the human and mouse sequences was approximately 70%. Dr. Hood stated that 70% is approximately the percentage of homology that many coding regions between mouse and man exhibit. Dr. Hood found this observation "a great surprise" because the T-cell receptor genes are a paradigm of the diversity genes, and he therefore did not expect to find a high level of homology between the mouse and human sequences.

Dr. Hood also reviewed data provided by Dr. Simons related to related to HLA genes. Dr. Hood stated that the "data provided by Malcolm Simons related to his discovery that one could use relatively short regions of non-coding sequences, on the order of one to two kilobasepairs, to define the corresponding coding region allele." Dr. Hood stated that Malcolm Simons' "data demonstrated that relatively short non-coding region sequences contained informative polymorphisms which can be used as the basis of an HLA typing system." Dr. Hood also saw the Declaration by Peter Gresshoff submitted with the Preliminary Amendment, described above.

Dr. Hood concluded:

"The HLA data and the NTS data indicate the presence of informative polymorphisms in non-coding regions in these vastly different types of genes from species that diverged tens of millions of years ago. In addition, the type of homology I found in sequencing non-coding regions of mouse and man in the Alpha Delta T-cell receptor is consistent with these findings. Therefore, I believe that informative polymorphisms which are indicative of linked alleles and haplotypes are present throughout the eukaryotic genome."

Dr. Hood's Declaration clearly evidences that an expert in genetics analyzing the data described above concluded that Dr. Simons' method is applicable to genes generally.

The criteria for evaluating declarations traversing rejections are set forth in M.P.E.P. 716. The criteria are (1) the declaration is timely filed; (2) the declaration must set forth facts, not merely conclusions and the facts must be pertinent to the rejection; (3) the declaration should be scrutinized closely and the facts presented weighed with care, particularly if the declarant is interested in the outcome of the case.

In response to the 35 U.S.C. §112 rejection, the Declaration of Dr. Gresshoff was submitted with a Preliminary Amendment. Therefore, the Declaration was timely. In his Declaration, Dr. Gresshoff described data he developed in studying the soybean NTS locus. Dr. Gresshoff described that he found that there were sequence polymorphisms in the intergenic region of the locus which indicated the allele of the gene. Therefore, Dr. Gresshoff provided facts, not merely conclusions. Applicant's Attorney notes that the M.P.E.P. requires that declarations present facts on which the conclusion are based. The declarations are not required to present raw data, such as the unpublished sequences described in Dr. Gresshoff's Declaration.

The facts presented by Dr. Gresshoff are pertinent to the rejection because the facts relate to whether non-coding region polymorphisms in non-HLA genes could be used to identify

alleles. The region described by Dr. Gresshoff is an intergenic region of non-coding DNA. Therefore, the facts are pertinent to the rejection. Finally, Dr. Gresshoff is neither a coinventor, nor an employee of the assignee of the application. He is a colleague of Dr. Simons. Therefore, the statements made by Dr. Gresshoff were not made to further any interests of Dr. Gresshoff.

Like the Declaration by Dr. Gresshoff, Dr. Hood's Declaration complies with the three criteria for evaluating declarations traversing rejections set forth in M.P.E.P. 716. First, the Declaration was timely filed in response to the first Office Action. The Declaration sets forth facts pertinent to the rejection, not merely conclusions. In particular, Dr. Hood described his data regarding a 100 kilobase region of the Alpha Delta T-cell receptor gene in both mouse and man. Although Dr. Hood did not present the complete sequences of the genes, he described facts such as the percentage of homology between the genes. The data is pertinent in that about ninety-five percent of the sequenced region was non-coding sequences. Finally, like Dr. Gresshoff, the statements made by Dr. Hood were not made to further any interests of Dr. Hood.

Dr. Hood concluded that the data indicated that informative polymorphisms which are indicative of linked alleles and haplotypes are present throughout the eukaryotic genome. Dr. Hood also concluded that the presence of non-coding region polymorphisms that are indicative of coding region polymorphisms (alleles) indicates that the phenomenon is present in eukaryotic genomes generally. The present method is based on the use of informative polymorphisms in non-coding regions to determine alleles and haplotypes.

In summary, there is clear evidence of record that the data indicates that such informative non-coding region polymorphisms are present throughout the eukaryotic genome.

The evidence clearly demonstrates that the present method is not limited to HLA genes but rather is applicable to eukaryotes generally. Since the application is fully enabled for the breadth of the claims, withdrawal of the rejection is respectfully requested.

Rejection under 35 U.S.C. §112, second paragraph  
(indefiniteness)

The rejection of Claims 1-16, 26, 27, 37, and 39-43 under 35 U.S.C. §112, second paragraph, as being indefinite is respectfully traversed.

Claim 7 was said to be indefinite for use of the term "genetic variation." The meaning of the phrase "genetic variation" in Claim 7 is clear. In addition, the meaning of the phrase was clarified in the Amendment filed May 6, 1991, in the parent application. Briefly, as described in the Amendment, the phrase refers to differences between DNA sequences of a genetic locus. Nucleotides in the sequences which differ are referred to as genetic variations in the sequence. That meaning is clear to one of skill in the art. In addition, the meaning of the phrase is described in the specification at page 8, line 35 through page 9, line 3. Exemplary genetic variations such as change in the length of the sequence, gain or loss of a restriction site or substitution of a nucleotide which result from insertions, deletions and substitutions in the sequences are described at pages 8 and 9 and exemplified throughout the application.

Claims 1-16 were rejected for being drawn to a method of detection without reciting any detection step because the claims lack "sufficient method steps." Independent Claims 1 and 7 have been amended to recite the step of detecting the allele. Claims 2-6 and 8-16 depend, directly or indirectly on Claims 1 or 7. If the Examiner does not believe this amendment

eliminates the basis of the rejection, clarification is requested.

Claim 26 was rejected for failing to recite any method step which calls for determining whether DNA from a sample is from a particular individual. Claim 27 has been amended in the same manner as Claims 1 and 7 to recite that the steps are performed the determination. It is believed that the amendment overcomes the rejection.

Claims 21 and 22-24 were rejected as confusing for stating that the primers were located in specified intervening sequences. The claims have been amended to state that the primer sites (the area of the target DNA to which a primer hybridizes, page 11, lines 17-18) are in the intervening sequences. Withdrawal of the rejection is requested.

Claims 22, 24, and 25 were said to be "confusing as it is not readily apparent where the method steps of said claims are to occur in the method of claim 21." This rejection is not understood. Claim 22 recites that "said amplification comprises . . . ." Step (a) of Claim 21 recites an amplification. Therefore, Claim 22 recites steps of the amplification of step (a) of Claim 21.

Claim 24 recites that "producing said RFLP fragment pattern comprises . . . ." Step (b) of Claim 21 recites producing RFLP patterns," and step (c) recites "producing RFLP patterns from said digest." Therefore, Claim 24 recites steps of steps (b) and (c) of Claim 21. Withdrawal of the rejection is respectfully requested.

Claim 25 depends on Claim 24 and recites that the fragments are separated using gel electrophoresis and visualized using a nucleotide-specific stain. Clearly, the fragments in Claim 24 are separated in step (ii) and visualized in step (iii). If the Examiner remains confused by the claims, a detailed explanation of the basis for the rejection is requested.

Claim 37 and dependent Claims 39-43 were rejected as being in incorrect Jepson format. Claim 37 has been amended to remove the Jepson format. Since the claim is now a standard method claim, there is no requirement that the claim recite all the steps of the method. In particular, Section 112, second paragraph, requires that the claims define the subject matter sought to be patented. The Board of Appeals stated:

The second paragraph of 35 U.S.C. §112 merely requires that an applicant set out and circumscribe a particular area with a reasonable degree of precision and particularity such that the metes and bounds of the claimed invention are reasonably set forth. (Ex parte Head 214 USPQ 551,552 (PTO Bd. App. 1981))

Similarly, the C.C.P.A. stated:

The first sentence of 35 U.S.C. §112 is essentially a requirement for precision and definiteness in claim language. If the scope of subject matter embraced by a claim is clear, and if the applicant has not otherwise indicated that he intends the claim to be of a different scope, the claim does particularly point out and distinctly claim the subject matter that the applicant regards as his invention. The requirement is that the language of the claims must make it clear what subject matter they encompass and thus make clear the subject matter from which they would preclude others. (In re Conley et al. 180 USPQ 454, 455 (CCPA 1974))

Section 112 does not require that the claims teach how to practice the invention. See In re Rainer et al. 134 USPQ 343 (CCPA 1962) and In re Johnson et al. 194 USPQ 187, 194 (1977). In In re Rainer et al., claims were rejected as unduly broad because the minimum energy level was not stated in the claims. The Court stated that the Board of Appeals found that reliance on the element stated in the claim would involve extensive experimentation for ascertaining the practical limits of operation. The Court stated:

It appears to us that the board is here confusing the requirements for claims with the function of specification. One does not look to the claims to find out how to practice inventions they define, but to specification. Here the "practical limits of operation" are set forth in the specification so as to eliminate any need for "extensive experimentation." (emphasis in original; 134 U.S.P.Q. at 346)

Therefore, the claims need to be enabled by the teachings of the specification. The claims do not need to recite all the

necessary steps to enable one to practice the claimed method. Since the rejection is based on the lack of reciting all the steps of the method, not on the failure of the specification to teach one of skill how to practice the method, the claims are definite and comply with the statutory requirements. Withdrawal of the rejection is respectfully requested.


In summary, the law makes no requirement that a method claim recite all the steps necessary to practice the method. The claim need only define the subject matter sought to be protected and distinguish the prior art. Since there are no art-based rejections and one of ordinary skill can clearly determine the metes and bounds of the claims and, therefore, determine when he is practicing the claimed subject matter, the claim fulfills the definiteness requirements of 35 U.S.C. §112, second paragraph.

Removal of all the 35 U.S.C. §112, second paragraph, rejections for indefiniteness is respectfully requested.

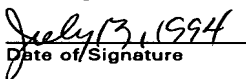
All of the rejections in the Office Action having been overcome, it is believed that the application is now in condition for allowance. Early notice to that effect is respectfully requested. If a telephone conference would expedite the prosecution of this application, the Examiner is requested to telephone and confer with the undersigned Attorney.

Date: July 13, 1994.

Respectfully submitted,

  
Laura Terlizzi  
Attorney for Applicant  
Reg. No. 31,307

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner of Patents and Trademarks, Washington, D.C., 20231, on July 13, 1994.

  
Date of Signature

  
Attorney for Applicant